# RECEIVED

## DEC 2 9 2003

### TECH CENTER 1600/2900

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RAW SEQUENCE LISTING              DATE: 12/19/2003
PATENT APPLICATION:  US/09/680,121C      TIME: 16:00:51

Input Set : A:\Amended Sequence Listing for 107-206-C-D.txt
Output Set: N:\CRF4\12192003\I680121C.raw
```

*p.6*

**ENTERED**

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 3 <110> APPLICANT: FRENCH, Cynthia K.
 4        YAMAMOTO, Karen K.
 5        EL SHAMI, A. Said
 7 <120> TITLE OF INVENTION: Prostate Cancer-Specific Marker
 9 <130> FILE REFERENCE: 107-206-C-D
11 <140> CURRENT APPLICATION NUMBER: 09/680,121C
12 <141> CURRENT FILING DATE: 2000-10-04
14 <150> PRIOR APPLICATION NUMBER: 60/041,246
15 <151> PRIOR FILING DATE: 1997-03-07
17 <150> PRIOR APPLICATION NUMBER: 60/047,811
18 <151> PRIOR FILING DATE: 1997-05-15
20 <150> PRIOR APPLICATION NUMBER: 09/036,315
21 <151> PRIOR FILING DATE: 1998-03-06
23 <150> PRIOR APPLICATION NUMBER: 09/535,597
24 <151> PRIOR FILING DATE: 2000-03-27
26 <150> PRIOR APPLICATION NUMBER: 09/680,121
27 <151> PRIOR FILING DATE: 2000-10-04
29 <160> NUMBER OF SEQ ID NOS: 27
31 <170> SOFTWARE: PatentIn Ver. 2.1
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 3891
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (151)..(1425)
42 <220> FEATURE:
43 <223> OTHER INFORMATION: product = Repro-PC-1.0
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48 cgttccgaaa gccggcgctt gagatccagg caagtgaatc cagccaggca gttttccctt 120
50 cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
51                                     Met Ala Pro Ile Thr Thr Ser Arg
52                                      1                   5
54 gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222
55 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
56       10                  15                  20
58 ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga 270
59 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
60   25                  30                  35                  40
62 aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318
63 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
64           45                  50                  55
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66 ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag    366
67 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
68              60                  65                  70
70 ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca    414
71 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
72          75                  80                  85
74 aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat    462
75 Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
76          90                  95                 100
78 ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat    510
79 Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
80 105                 110                 115                 120
82 gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct    558
83 Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
84              125                 130                 135
86 gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag    606
87 Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
88              140                 145                 150
90 aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa    654
91 Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
92          155                 160                 165
94 gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat    702
95 Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp
96      170                 175                 180
98 gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca    750
99 Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro
100 185                 190                 195                 200
102 gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat   798
103 Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp
104              205                 210                 215
106 cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa   846
107 Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln
108              220                 225                 230
110 atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt   894
111 Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe
112              235                 240                 245
114 tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att   942
115 Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile
116      250                 255                 260
118 gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga   990
119 Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg
120 265                 270                 275                 280
122 aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc   1038
123 Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
124              285                 290                 295
126 tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga   1086
127 Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
128              300                 305                 310
130 cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa   1134
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131 His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
132         315             320             325
134 gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat    1182
135 Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
136     330             335             340
138 gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt    1230
139 Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
140 345             350             355             360
142 gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt    1278
143 Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
144             365             370             375
146 ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc    1326
147 Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
148             380             385             390
150 ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc    1374
151 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
152             395             400             405
154 tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat    1422
155 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
156     410             415             420
158 ggt tagcatccta gccgtgagtt ggaacttaaa ggtttttact aggcaaggag         1475
159 Gly
160 425
162 aaattttctt tctttctata ttggattgca agcttgggaa atcaagctac ctttttgttg 1535
164 ttgttgttgt tgctagaaat ggattgaatt agtagaccag aaagtaactt caaatgtgta 1595
166 ttatgataat ttccctattt attagaagag ttggataaat tttcataaga tattcaatat 1655
168 ctccttcaga ttaccagtga tataactagg aatagtcaga cattttatga atactgtgcc 1715
170 agaatcccaa attataaatg tgacaatctc attggaacat gtcacaaaaa gttaatgtga 1775
172 ttaagattta aaaacgaaaa gtatgccttg ccttgtgaaa atttatccat ttatcttcag 1835
174 gttgggggaa atcaattttt ctttaatcca aagatactaa aaaaatgtcc tccagtttgt 1895
176 atttattaat tctgtcatgt gcaaatggtt gtcctgcata taaaagtatc tggtcatttc 1955
178 agtttggttt gtaattattt gatgcaattt tatcataaga gtaactcaga ttcatttcaa 2015
180 aaggacagtg aacaagctga gaaattattt tatcaaaggg ctgagttgag aacactgtgg 2075
182 ctgaaatata attttctcc ccctaaggt tacatgtgag tcaaaatttt gtaaaatata 2135
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206 gaattattaa atatgcaagt tagaaattaa gtctactgaa aaatttacat tttgagtcag 2855
208 gttttgtgtc agtactttag cagtttttga gaatgtgttt gatatcacag tgtttgtaaa 2915
210 ttctatgaaa aatgcatttt ccaaacaact tatacatgct ttttatgact atgcctaatg 2975
212 taaagaaaat gtattacatt ctgtatgtac aaagattaaa aatcaacctc tttttgtgc   3035
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214 tttaaaatga ctttgggatt aaaaaagcat atttcccaat cattgtcttc attccactac 3095
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218 ctgtagtagg tgtgtagttt ggggaagtca aatggccatt ttatgtatgt gcatttggta 3215
220 tcatgggccg tggaacagaa tatatgttgg acctctgaaa agttgtaagg ggccaaatct 3275
222 aagtattctt cacggcagcc agaagttaat ggtggtagca gctgaggtat ggttgttgga 3335
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232 ttttagaatg tattacaata tcaatgtgaa tatcttgaat cctgttacaa atcctgcact 3635
234 gtattaaaca tgtaaattaa ttgtttgtct gattagccaa tctcaccacc caaatgggga 3695
236 ggtatacatg tttgaagaac gtgtaactcg gtaattgatt tgttctgatg ttgtaactca 3755
238 atagaagtgt tttggaagga agcatggtgt gtgagacagt gtctgttctt ttgtgccagc 3815
240 tctgtatgat gtttgtaaga ccatgtttgt aagacatgaa taaattgctg cttttgccca 3875
242 aaaaaaaaaa aaaaaa                                             3891
245 <210> SEQ ID NO: 2
246 <211> LENGTH: 425
247 <212> TYPE: PRT
248 <213> ORGANISM: Homo sapiens
> 249 <220> FEATURE:
250 <223> OTHER INFORMATION: product = Repro-PC-1.0
252 <400> SEQUENCE: 2
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257             20                  25                  30
259 Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
260             35                  40                  45
262 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
263         50                  55                  60
265 Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
266  65                  70                  75                  80
268 Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
269             85                  90                  95
271 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
272             100                 105                 110
274 Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
275             115                 120                 125
277 Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
278         130                 135                 140
280 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
281 145                 150                 155                 160
283 Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
284             165                 170                 175
286 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
287             180                 185                 190
289 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
290             195                 200                 205
292 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
```

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293      210                  215                  220
295 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
296 225                  230                  235                  240
298 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
299                  245                  250                  255
301 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
302                  260                  265                  270
304 Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
305           275                  280                  285
307 Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
308      290                  295                  300
310 Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
311 305                  310                  315                  320
313 Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
314                  325                  330                  335
316 Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
317           340                  345                  350
319 Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
320           355                  360                  365
322 Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
323      370                  375                  380
325 Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
326 385                  390                  395                  400
328 Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile
329                  405                  410                  415
331 Ala Lys Trp His Val Leu Cys Asp Gly
332                  420                  425
336 <210> SEQ ID NO: 3
337 <211> LENGTH: 21
338 <212> TYPE: DNA
339 <213> ORGANISM: Homo sapiens
341 <220> FEATURE:
342 <221> NAME/KEY: misc_feature
343 <222> LOCATION: (1)..(21)
344 <223> OTHER INFORMATION: 5' oligo (109) Upper Primer
346 <400> SEQUENCE: 3
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351 <211> LENGTH: 30
352 <212> TYPE: DNA
353 <213> ORGANISM: Homo sapiens
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (1)..(30)
358 <223> OTHER INFORMATION: 3' oligo (3489) Lower Primer
360 <400> SEQUENCE: 4
361 ttcctttgtt gtttcttttc tcttttctga                           30
364 <210> SEQ ID NO: 5
365 <211> LENGTH: 425
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RAW SEQUENCE LISTING ERROR SUMMARY     DATE: 12/19/2003
PATENT APPLICATION:  US/09/680,121C     TIME: 16:00:52

Input Set : **A:\Amended Sequence Listing for 107-206-C-D.txt**
Output Set: **N:\CRF4\12192003\I680121C.raw**

<u>ase Note:</u>
 of n and/or Xaa have been detected in the Sequence Listing. Please review the
uence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

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#:11; Xaa Pos. 1,2,3,4,5,6,7,8
#:12; Xaa Pos. 1,2,3,4,5,6,7,8,9
#:13; Xaa Pos. 1,2,3,4,5,6
#:14; Xaa Pos. 1,2,3,4,5,6,7
#:15; Xaa Pos. 1,2,3,4,5,6,7,8,9
#:16; Xaa Pos. 1,2,3,4,5,6,7,8,9,10
#:17; Xaa Pos. 1,2,3,4,5,6,7,8
#:18; Xaa Pos. 1,2,3,4,5,6,7,8,9
#:19; Xaa Pos. 1,2,3,4,5,6,7,8,9
#:20; Xaa Pos. 1,2,3,4,5,6,7,8,9,10
#:27; Xaa Pos. 5
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**VERIFICATION SUMMARY**                    DATE: 12/19/2003
PATENT APPLICATION: **US/09/680,121C**      TIME: 16:00:52

Input Set : **A:\Amended Sequence Listing for 107-206-C-D.txt**
Output Set: **N:\CRF4\12192003\I680121C.raw**

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49 M:283 W: Missing Blank Line separator, <220> field identifier
46 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
55 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
64 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
83 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
92 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
01 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
10 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
20 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
49 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
77 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
86 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
96 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
05 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
14 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
24 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
43 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
52 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
71 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
80 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
89 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
08 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
17 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
54 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
63 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
72 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
91 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
000 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
009 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
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